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Canton MO

Corresponding Faculty Member: Esa Seegulam (mseegulam@culver.edu)



Drew N Klocke

Isolation and Characterization of the Bacteriophage AvadaKedavra

Muhammad E Seegulam, Zachary M English, Alexander R Heaney, Julianna N Hollman, Bryan J Hunter, Drew N Klocke

In this experiment we sought to isolate and characterize a novel bacteriophage from an environmental sample. A soil sample was collected from the Northeast Missouri region and putative phages amplified using M. smegmatis mc2155 as a bacterial host. The sample was subjected to several rounds of purification with the aim of isolating a novel bacteriophage. The presence of bacteriophage was inferred by the formation of clearings, or plaques, on bacterial lawns that had been infected with samples containing the putative phage. Three new phages were discovered by the current cohort: JoeDirt26, SchmutzDaCat, and Pass. Genomic analysis was conducted on bacteriophage Avadakedavra isolated by the 2015 cohort. The Avadakedavra genome was 73721 base pairs long, with cluster L assignment and subcluster L1. Minor tail protein, membrane domain protein, and capsid maturation protease were among the known products encoded by the 121 features identified in a preliminary analysis of the Avadakedavra genome, while 65 were found to have no known function. Also encoded in the Avadakedavra genome is a single tRNA, tRNA-Cys(TGC). The programs used for annotation include DNA Master, Phamerator, Starterator, HHpred, NCBI BLAST and PECAAN.